RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/562,469_
Source: _IFWD_
Date Processed by STIC: _07/07/2006_

ENTERED

RAW SEQUENCE LISTING   DATE: 07/07/2006
PATENT APPLICATION: US/10/562,469 TIME: 14:20:05

Input Set : E:\405uspc.app.txt
Output Set: N:\CRF4\07072006\J562469.raw

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 3 <110> APPLICANT: Masato MIYAKE
 4        Tomohiro YOSHIKAWA
 5        Jun MIYAKE
 7 <120> TITLE OF INVENTION: Digital cell
 9 <130> FILE REFERENCE: 690121.405USPC
11 <140> CURRENT APPLICATION NUMBER: US 10/562,469
C--> 12 <141> CURRENT FILING DATE: 2005-12-22
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/009404
15 <151> PRIOR FILING DATE: 2004-06-25
17 <150> PRIOR APPLICATION NUMBER: JP 2003-289469
18 <151> PRIOR FILING DATE: 2003-08-07
20 <150> PRIOR APPLICATION NUMBER: JP 2003-181915
21 <151> PRIOR FILING DATE: 2003-06-25
23 <160> NUMBER OF SEQ ID NOS: 50
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1929
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(1929)
35 <223> OTHER INFORMATION: fibronectin 1
38 <400> SEQUENCE: 1
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40 Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys
41 1               5                   10                  15
43 ctg ggg aca gcg gtg ccc tcc acg gga gcc tcg aag agc aag agg cag       96
44 Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln
45              20                  25                  30
47 gct cag caa atg gtt cag ccc cag tcc ccg gtg gct gtc agt caa agc      144
48 Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser
49          35                  40                  45
51 aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa cag      192
52 Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln
53      50                  55                  60
55 tgg gag cgg acc tac cta ggc aat gcg ttg gtt tgt act tgt tat gga      240
56 Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly
57 65                  70                  75                  80
59 gga agc cga ggt ttt aac tgc gag agt aaa cct gaa gct gaa gag act      288
60 Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr
61              85                  90                  95
63 tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act tat      336
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 64 Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr
 65             100             105             110
 67 gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg gct     384
 68 Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala
 69 ·         115             120             125
 71 ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa ggg     432
 72 Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly
 73         130             135             140
 75 ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag act     480
 76 Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr
 77 145             150             155             160
 79 ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga gaa     528
 80 Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu
 81             165             170             175
 83 tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct ggg     576
 84 Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly
 85             180             185             190
 87 act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc tgg     624
 88 Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp
 89         195             200             205
 91 atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc act     672
 92 Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr
 93     210             215             220
 95 tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc tat     720
 96 Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr
 97 225             230             235             240
 99 aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg ctc     768
100 Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu
101             245             250             255
103 cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag agg     816
104 Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg
105             260             265             270
107 cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc gat     864
108 His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp
109         275             280             285
111 gtt cgt gca gct gtt tac caa ccg cag cct cac ccc cag cct cct ccc     912
112 Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro
113     290             295             300
115 tat ggc cac tgt gtc aca gac agt ggt gtg gtc tac tct gtg ggg atg     960
116 Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met
117 305             310             315             320
119 cag tgg ctg aag aca caa gga aat aag caa atg ctt tgc acg tgc ctg    1008
120 Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu
121             325             330             335
123 ggc aac gga gtc agc tgc caa gag aca gct gta acc cag act tac ggt    1056
124 Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly
125             340             345             350
127 ggc aac tca aat gga gag cca tgt gtc tta cca ttc acc tac aat ggc    1104
128 Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly
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Input Set : **E:\405uspc.app.txt**
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129        355                    360                    365
131 agg acg gac agc aca act tcg aat tat gag cag gac cag aaa tac tct      1152
132 Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser
133        370                    375                    380
135 ttc tgc aca gac cac act gtt ttg gtt cag act cga gga gga aat tcc      1200
136 Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser
137 385              ..    .390       .              395                    400
139 aat ggt gcc ttg tgc cac ttc ccc ttc cta tac aac aac cac aat tac      1248
140 Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr
141             405                    410                    415
143 act gat tgc act tct gag ggc aga aga gac aac atg aag tgg tgt ggg      1296
144 Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly
145             420                    425                    430
147 acc aca cag aac tat gat gcc gac cag aag ttt ggg ttc tgc ccc atg      1344
148 Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met
149             435                    440                    445
151 gct gcc cac gag gaa atc tgc aca acc aat gaa ggg gtc atg tac cgc      1392
152 Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg
153        450                    455                    460
155 att gga gat cag tgg gat aag cag cat gac atg ggt cac atg atg agg      1440
156 Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg
157 465                    470                    475                    480
159 tgc acg tgt gtt ggg aat ggt cgt ggg gaa tgg aca tgc att gcc tac      1488
160 Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr
161             485                    490                    495
163 tcg cag ctt cga gat cag tgc att gtt gat gac atc act tac aat gtg      1536
164 Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val
165             500                    505                    510
167 aac gac aca ttc cac aag cgt cat gaa gag ggg cac atg ctg aac tgt      1584
168 Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys
169             515                    520                    525
171 aca tgc ttc ggt cag ggt cgg ggc agg tgg aag tgt gat ccc gtc gac      1632
172 Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp
173        530                    535                    540
175 caa tgc cag gat tca gag act ggg acg ttt tat caa att gga gat tca      1680
176 Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser
177 545                    550                    555                    560
179 tgg gag aag tat gtg cat ggt gtc aga tac cag tgc tac tgc tat ggc      1728
180 Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly
181             565                    570                    575
183 cgt ggc att ggg gag tgg cat tgc caa cct tta cag acc tat cca agc      1776
184 Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser
185             580                    585                    590
187 tca agt ggt cct gtc gaa gta ttt atc act gag act ccg agt cag ccc      1824
188 Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro
189             595                    600                    605
191 aac tcc cac ccc atc cag tgg aat gca cca cag cca tct cac att tcc      1872
192 Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser
193        610                    615                    620
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RAW SEQUENCE LISTING   DATE: 07/07/2006
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Input Set : E:\405uspc.app.txt
Output Set: N:\CRF4\07072006\J562469.raw

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195 aag tac att ctc agg tgg aga cct gtg agt atc cca ccc aga aac ctt    1920
196 Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn Leu
197 625                 630             635             640
199 gga tac tga                                                        1929
200 Gly Tyr
204 <210> SEQ ID NO: 2
205 <211> LENGTH: 642
206 <212> TYPE: PRT
207 <213> ORGANISM: Homo sapiens
209 <400> SEQUENCE: 2
211 Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys
212 1               5               10              15
215 Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln
216             20              25              30
219 Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser
220             35              40              45
223 Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln
224     50              55              60
227 Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly
228 65              70              75              80
231 Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr
232             85              90              95
235 Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr
236             100             105             110
239 Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala
240         115             120             125
243 Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly
244     130             135             140
247 Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr
248 145             150             155             160
252 Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu
253             165             170             175
256 Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly
257             180             185             190
260 Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp
261         195             200             205
264 Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr
265     210             215             220
268 Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr
269 225             230             235             240
272 Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu
273             245             250             255
276 Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg
277             260             265             270
280 His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp
281         275             280             285
284 Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro
285     290             295             300
288 Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met
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Input Set : E:\405uspc.app.txt
Output Set: N:\CRF4\07072006\J562469.raw

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289 305                  310              315                  320
292 Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu
293             325              330              335
296 Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly
297         340              345              350
300 Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly
301         355          360              365
304 Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser
305     370              375              380
308 Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser
309 385              390              395              400
312 Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr
313             405              410              415
316 Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly
317         420              425              430
320 Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met
321         435              440              445
324 Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg
325     450              455              460
328 Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg
329 465              470              475              480
332 Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr
333             485              490              495
336 Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val
337             500              505              510
340 Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys
341         515              520              525
344 Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp
345     530              535              540
348 Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser
349 545              550              555              560
352 Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly
353             565              570              575
356 Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser
357         580              585              590
360 Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro
361         595              600              605
364 Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser
365     610              615              620
368 Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn Leu
369 625              630              635              640
372 Gly Tyr
376 <210> SEQ ID NO: 3
377 <211> LENGTH: 1437
378 <212> TYPE: DNA
379 <213> ORGANISM: Mus musculus
381 <220> FEATURE:
382 <221> NAME/KEY: CDS
383 <222> LOCATION: (1)..(1437)
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/07/2006
PATENT APPLICATION: US/10/562,469   TIME: 14:20:06

Input Set : **E:\405uspc.app.txt**
Output Set: **N:\CRF4\07072006\J562469.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 99
Seq#:31; N Pos. 3
Seq#:33; N Pos. 15
Seq#:35; N Pos. 108
Seq#:37; N Pos. 940,1083
Seq#:37; Xaa Pos. 286
Seq#:38; Xaa Pos. 286

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:12; Line(s) 4237

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:12,47,48

VERIFICATION SUMMARY   DATE: 07/07/2006
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Input Set : **E:\405uspc.app.txt**
Output Set: **N:\CRF4\07072006\J562469.raw**

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:4240 M:112 C: (48) String data converted to lower case,
L:4661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:60
L:5958 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:6177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:6380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:60
L:6672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:929
L:6673 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:977
L:6684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:1080
L:6767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:272